



SEQUENCE LISTING

sub
G1

<110> LONGACRE-ANDRE, SHIRLEY
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NATO, FARIDABNO
BARNWELL, JOHN
MENDIS, KAMINI

<120> RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF PLASMODIUM MSP-1

<130> 0660-0135-0XCIP

<140> 09/134,333

<141> 1998-08-14

<150> PCT/FR97/00290

<151> 1997-02-14

<150> FR96/01822

<151> 1996-02-14

<160> 15

<170> PatentIn version 3.1

<210> 1

<211> 291

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA

<220>

<221> CDS

<222> (1)..(291)

<223>

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gaa ttc aac atc tcg cag cac caa tgc gtc aaa aaa caa tgt ccc gag 48
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu
1 5 10 15

aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 96
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
20 25 30

ctg ctg aac tac aaa cag gag ggc gac aag tgc gtc gag aac ccc aac 144
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
35 40 45

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
50 55 60

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys

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TECH CENTER 1600/2900

Sub
GI

F1

Sub
G!
cctgattctt atccactttt cgatggtatt ttctgcagt

279

<210> 4
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA

<220>
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<222> (1) .. (354)
<223>

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gaa ttc aac atc tcg cag cac caa tgc gtg aaa aaa caa tgt ccc gag 48
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu
1 5 10 15

aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 96
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
20 25 30

ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac 144
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
35 40 45

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
50 55 60

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
65 70 75 80

acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc tcc 288
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser
85 90 95

tct aac ttc ttg ggc atc tcg ttc ttg ttg atc ctc atg ttg atc ttg 336
Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met Leu Ile Leu
100 105 110

tac agc ttc att taa taa 354
Tyr Ser Phe Ile
115

F1
<210> 5
<211> 116
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<213> Artificial Sequence

<220>
<223> synthetic peptide

Sub
GI
<400> 5

Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu
1 5 10 15

Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
20 25 30

Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
35 40 45

Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
50 55 60

Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
65 70 75 80

Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser
85 90 95

Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met Leu Ile Leu
100 105 110

Tyr Ser Phe Ile
115

<210> 6

<211> 342

<212> DNA

<213> Plasmodium falciparum

<400> 6

aacatttcac aacaccaatg cgtaaaaaaa caatgtccag aaaattctgg atgtttcaga 60

catttagatg aaagagaaga atgtaaatgt ttattaaatt acaaacaaga aggtgataaa 120

tgtgttgaaa atccaaatcc tacttgtaac gaaaataatg gtggatgtga tgcagatgcc 180

aaatgtaccg aagaagattc aggtagcaac ggaaagaaaa tcacatgtga atgtactaaa 240

cctgattcct atccactttt cgatgggtatt ttctgcagtt cctctaactt cttaggaata 300

tcattcttat taatactcat gttaatatta tacagtttca tt 342

<210> 7

<211> 387

<212> DNA

Sub
G1
<213> Plasmodium falciparum

<220>

<221> CDS

<222> (1)..(387)

<223>

<400> 7

atg aag gcg cta ctc ttt ttg ttc tct ttc att ttt ttc gtt acc aaa 48
Met Lys Ala Leu Leu Phe Leu Phe Ser Phe Ile Phe Phe Val Thr Lys
1 5 10 15

tgt caa tgt gaa aca gaa agt tat aag cag ctt gta gcc aac gtg gac 96
Cys Gln Cys Glu Thr Glu Ser Tyr Lys Gln Leu Val Ala Asn Val Asp
20 25 30

gaa ttc aac atc tcg cag cac caa tgc gtg aaa aaa caa tgt ccc gag 144
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu
35 40 45

aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 192
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
50 55 60

ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac 240
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
65 70 75 80

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 288
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
85 90 95

acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 336
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
100 105 110

acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc taa 384
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
115 120 125

taa 387

<210> 8

<211> 127

<212> PRT

<213> Plasmodium falciparum

<400> 8

Met Lys Ala Leu Leu Phe Leu Phe Ser Phe Ile Phe Phe Val Thr Lys
1 5 10 15

Cys Gln Cys Glu Thr Glu Ser Tyr Lys Gln Leu Val Ala Asn Val Asp
20 25 30

sub
GI
Glu Phe Asn Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu
35 40 45

Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys
50 55 60

Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn
65 70 75 80

Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys
85 90 95

Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys
100 105 110

Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
115 120 125

<210> 9
<211> 330
<212> DNA
<213> Plasmodium falciparum

<220>
<221> CDS
<222> (1)..(330)
<223>

<400> 9
gaa aca gaa agt tat aag cag ctt gta gcc aac gtg gac gaa ttc aac 48
Glu Thr Glu Ser Tyr Lys Gln Leu Val Ala Asn Val Asp Glu Phe Asn
1 5 10 15

atc tcg cag cac caa tgc gtg aaa aaa caa tgt ccc gag aac tct ggc 96
Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu Asn Ser Gly
20 25 30

tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt ctg ctg aac 144
Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys Leu Leu Asn
35 40 45

tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac ccg acc tgt 192
Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro Thr Cys
50 55 60

F1
aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc acc gag gag 240
Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys Thr Glu Glu
65 70 75 80

gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt acc aaa ccc 288

sub
G1
Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys Thr Lys Pro
85 90 95

gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc taa taa
Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
100 105

330

<210> 10
<211> 108
<212> PRT
<213> Plasmodium falciparum

<400> 10

Glu Thr Glu Ser Tyr Lys Gln Leu Val Ala Asn Val Asp Glu Phe Asn
1 5 10 15

Ile Ser Gln His Gln Cys Val Lys Lys Gln Cys Pro Glu Asn Ser Gly
20 25 30

Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys Leu Leu Asn
35 40 45

Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro Thr Cys
50 55 60

Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys Thr Glu Glu
65 70 75 80

Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys Thr Lys Pro
85 90 95

Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser
100 105

<210> 11
<211> 379
<212> PRT
<213> Plasmodium cynomolgi

<220>
<221> MISC_FEATURE
<222> (1)..(139)
<223> REGION I

F1
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<222> (140)..(177)

Sub
G1

<223> REGION II

<220>

<221> MISC_FEATURE

<222> (178)..(282)

<223> REGION III

<220>

<221> MISC_FEATURE

<222> (283)..(379)

<223> REGION IV

<400> 11

Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Ile
1 5 10 15

Val Pro Gln Gly Ile Asn Glu Tyr Asp Val Val Tyr Ile Lys Pro Leu
20 25 30

Ala Gly Met Tyr Lys Thr Ile Lys Lys Pro Leu Glu Asn His Val Asn
35 40 45

Ala Leu Asn Thr Asn Ile Ile Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60

Arg Asn Tyr Phe Leu Asp Val Leu Asn Ser Asp Leu Asn Pro Tyr Ser
65 70 75 80

Ile Pro His Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu
85 90 95

Asp Leu Glu Lys Lys Lys Leu Leu Gly Ser Tyr Lys Tyr Ile Gly Ala
100 105 110

Ser Val Asp Lys Asp Met Val Thr Ala Asn Asp Gly Leu Ala Tyr Tyr
115 120 125

Gln Lys Met Gly Asp Leu Tyr Lys Lys His Leu Asp Glu Val Asn Ala
130 135 140

Cys Ile Lys Glu Val Glu Ala Asn Ile Asn Lys His Asp Glu Glu Ile
145 150 155 160

Sub
GI
Lys Lys Ile Gly Ser Glu Ala Ser Lys Ala Asn Asp Lys Asn Gln Leu
165 170 175

Asn Ala Lys Lys Glu Glu Leu Gln Lys Tyr Leu Pro Phe Leu Ser Ser
180 185 190

Ile Gln Lys Glu Tyr Ser Thr Leu Val Asn Lys Val His Ser Tyr Thr
195 200 205

Asp Thr Leu Lys Lys Ile Ile Asn Asn Cys Gln Ile Glu Lys Lys Glu
210 215 220

Thr Glu Thr Ile Val Asn Lys Leu Glu Asp Tyr Ser Lys Met Asp Glu
225 230 235 240

Glu Leu Asp Val Tyr Lys Gln Ser Lys Lys Glu Asp Asp Val Lys Ser
245 250 255

Ser Gly Leu Leu Glu Lys Leu Met Asn Ser Lys Leu Ile Asn Gln Glu
260 265 270

Glu Ser Lys Lys Ala Leu Ser Glu Leu Leu Asn Val Gln Thr Gln Met
275 280 285

Leu Asn Met Ser Ser Glu His Arg Cys Ile Asp Thr Asn Val Pro Glu
290 295 300

Asn Ala Ala Cys Tyr Arg Tyr Leu Asp Gly Thr Glu Glu Trp Arg Cys
305 310 315 320

Leu Leu Tyr Phe Lys Glu Asp Ala Gly Lys Cys Val Pro Ala Pro Asn
325 330 335

Met Thr Cys Lys Asp Lys Asn Gly Gly Cys Ala Pro Glu Ala Glu Cys
340 345 350

Lys Met Asn Asp Lys Asn Glu Ile Val Cys Lys Cys Thr Lys Glu Gly
355 360 365

FI
Ser Glu Pro Leu Phe Glu Gly Val Phe Cys Ser
370 375

<210> 12

Sub
G1
<211> 380
<212> PRT
<213> Plasmodium vivax-like sp.

<220>
<221> MISC_FEATURE
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<223> REGION I

<220>
<221> MISC_FEATURE
<222> (141)..(178)
<223> REGION II

<220>
<221> MISC_FEATURE
<222> (179)..(283)
<223> REGION III

<220>
<221> MISC_FEATURE
<222> (284)..(380)
<223> REGION IV

<400> 12

Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Leu
1 5 10 15

Val Pro Ala Gly Ile Ser Asp Tyr Asp Val Val Tyr Leu Lys Pro Leu
20 25 30

Ala Gly Met Tyr Lys Thr Ile Lys Lys Gln Leu Glu Asn His Val Asn
35 40 45

Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60

Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys
65 70 75 80

Tyr Ser Pro Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu
85 90 95

Asp Leu Glu Lys Lys Lys Lys Leu Leu Gly Ser Tyr Lys Tyr Ile Gly
100 105 110

~~Ala Ser Ile Asp Lys Asp Leu Ala Thr Ala Asn Asp Gly Val Thr Tyr
 115 120 125
 Tyr Asn Lys Met Gly Glu Leu Tyr Lys Thr His Leu Thr Ala Val Asn
 130 135 140
 Glu Glu Val Lys Lys Val Glu Ala Asp Ile Lys Ala Glu Asp Asp Lys
 145 150 155 160
 Ile Lys Lys Ile Gly Ser Asp Ser Thr Lys Thr Thr Glu Lys Thr Gln
 165 170 175
 Ser Met Ala Lys Lys Ala Glu Leu Glu Lys Tyr Leu Pro Phe Leu Asn
 180 185 190
 Ser Leu Gln Lys Glu Tyr Glu Ser Leu Val Ser Lys Val Asn Thr Tyr
 195 200 205
 Thr Asp Asn Leu Lys Lys Val Ile Asn Asn Cys Gln Leu Glu Lys Lys
 210 215 220
 Glu Ala Glu Ile Thr Val Lys Lys Leu Gln Asp Tyr Asn Lys Met Asp
 225 230 235 240
 Glu Lys Leu Glu Glu Tyr Lys Lys Ser Glu Lys Lys Asn Glu Val Lys
 245 250 255
 Ser Ser Gly Leu Leu Glu Lys Leu Met Lys Ser Lys Leu Ile Lys Glu
 260 265 270
 Asn Glu Ser Lys Glu Ile Leu Ser Gln Leu Leu Asn Val Gln Thr Gln
 275 280 285
 Leu Leu Thr Met Ser Ser Glu His Thr Cys Ile Asp Thr Asn Val Pro
 290 295 300
 Asp Asn Ala Ala Cys Tyr Arg Tyr Leu Asp Gly Thr Glu Glu Trp Arg
 305 310 315 320
 Cys Leu Leu Thr Phe Lys Glu Glu Gly Gly Lys Cys Val Pro Ala Ser
 325 330 335~~

Asn Val Thr Cys Lys Asp Asn Asn Gly Gly Cys Ala Pro Glu Ala Glu
340 345 350

Cys Lys Met Thr Asp Ser Asn Lys Ile Val Cys Lys Cys Thr Lys Glu
355 360 365

Gly Ser Glu Pro Leu Phe Glu Gly Val Phe Cys Ser
370 375 380

<210> 13
<211> 380
<212> PRT
<213> Plasmodium vivax-like sp.

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<221> MISC_FEATURE
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<223> REGION IV

<400> 13

Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Leu
1 5 10 15

Val Pro Ala Gly Ile Ser Asp Tyr Asp Val Val Tyr Leu Lys Pro Leu
20 25 30

Ala Gly Met Tyr Lys Thr Ile Lys Lys Gln Leu Glu Asn His Val Asn
35 40 45

Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60

Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys
 65 70 75 80
 Tyr Ser Ser Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu
 85 90 95
 Asp Leu Glu Lys Lys Lys Lys Leu Ile Gly Ser Tyr Lys Tyr Ile Gly
 100 105 110
 Ala Ser Ile Asp Met Asp Leu Ala Thr Ala Asn Asp Gly Val Thr Tyr
 115 120 125
 Tyr Asn Lys Met Gly Glu Leu Tyr Lys Thr His Leu Asp Gly Val Lys
 130 135 140
 Thr Glu Ile Lys Lys Val Glu Asp Asp Ile Lys Lys Gln Asp Glu Glu
 145 150 155 160
 Leu Lys Lys Leu Gly Asn Val Asn Ser Gln Asp Ser Lys Lys Asn Glu
 165 170 175
 Phe Ile Ala Lys Lys Ala Glu Leu Glu Lys Tyr Leu Pro Phe Leu Asn
 180 185 190
 Ser Leu Gln Lys Glu Tyr Glu Ser Leu Val Ser Lys Val Asn Thr Tyr
 195 200 205
 Thr Asp Asn Leu Lys Lys Val Ile Asn Asn Cys Gln Leu Glu Lys Lys
 210 215 220
 Glu Ala Glu Ile Thr Val Lys Lys Leu Gln Asp Tyr Asn Lys Met Asp
 225 230 235 240
 Glu Lys Leu Glu Glu Tyr Lys Lys Ser Glu Lys Lys Asn Glu Val Lys
 245 250 255
 Ser Ser Gly Leu Leu Glu Lys Leu Met Lys Ser Lys Leu Ile Lys Glu
 260 265 270
 Asn Glu Ser Lys Glu Ile Leu Ser Gln Leu Leu Asn Val Gln Thr Gln
 275 280 285

Leu Leu Thr Met Ser Ser Glu His Thr Cys Ile Asp Thr Asn Val Pro
290 295 300

Asp Asn Ala Ala Cys Tyr Arg Tyr Leu Asp Gly Thr Glu Glu Trp Arg
305 310 315 320

Cys Leu Leu Thr Phe Lys Glu Glu Gly Gly Lys Cys Val Pro Ala Ser
325 330 335

Asn Val Thr Cys Lys Asp Asn Asn Gly Gly Cys Ala Pro Glu Ala Glu
340 345 350

Cys Lys Met Thr Asp Ser Asn Lys Ile Val Cys Lys Cys Thr Lys Glu
355 360 365

Gly Ser Glu Pro Leu Phe Glu Gly Val Phe Cys Ser
370 375 380

<210> 14
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<213> Artificial Sequence

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<223> synthetic polypeptide

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<222> (1)..(115)
<223> REGION I

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<222> (116)..(125)
<223> REGION II

<220>
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<222> (126)..(197)
<223> REGION III

<220>
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<223> REGION IV

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Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Val
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Pro Gly Ile Tyr Asp Val Val Tyr Lys Pro Leu Ala Gly Met Tyr Lys
20 25 30

Thr Ile Lys Lys Leu Glu Asn His Val Asn Ala Asn Thr Asn Ile Asp
35 40 45

Met Leu Asp Ser Ala Leu Lys Lys Ala Asn Tyr Phe Leu Val Leu Asn
50 55 60

Ser Asp Leu Asn Pro Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys
65 70 75 80

Leu Leu Asp Leu Glu Lys Lys Lys Leu Gly Ser Tyr Lys Tyr Ile Gly
85 90 95

Ala Ser Asp Asp Thr Ala Asn Asp Gly Tyr Tyr Lys Met Gly Leu Tyr
100 105 110

Lys His Leu Val Lys Val Glu Ile Asp Lys Lys Gly Lys Ala Lys Lys
115 120 125

Glu Leu Lys Tyr Leu Pro Phe Leu Ser Gln Lys Glu Tyr Leu Val Lys
130 135 140

Val Tyr Thr Asp Leu Lys Lys Ile Asn Asn Cys Gln Glu Lys Lys Glu
145 150 155 160

Glu Val Lys Leu Asp Tyr Lys Met Asp Glu Leu Tyr Lys Ser Lys Val
165 170 175

Lys Ser Ser Gly Leu Leu Glu Lys Leu Met Ser Lys Leu Ile Glu Ser
180 185 190

Lys Leu Ser Leu Leu Asn Val Gln Thr Gln Leu Met Ser Ser Glu His
195 200 205

Cys Ile Asp Thr Asn Val Pro Asn Ala Ala Cys Tyr Arg Tyr Leu Asp
210 215 220

*Sub
GI
Cont*

Gly Thr Glu Glu Trp Arg Cys Leu Leu Phe Lys Glu Gly Lys Cys Val
225 230 235 240

Pro Ala Asn Thr Cys Lys Asp Asn Gly Gly Cys Ala Pro Glu Ala Glu
245 250 255

Cys Lys Met Asp Asn Ile Val Cys Lys Cys Thr Lys Glu Gly Ser Glu
260 265 270

Pro Leu Phe Glu Gly Val Phe Cys Ser
275 280

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 15

Leu Asn Val Gln Thr Gln
1 5